

Fig. 1

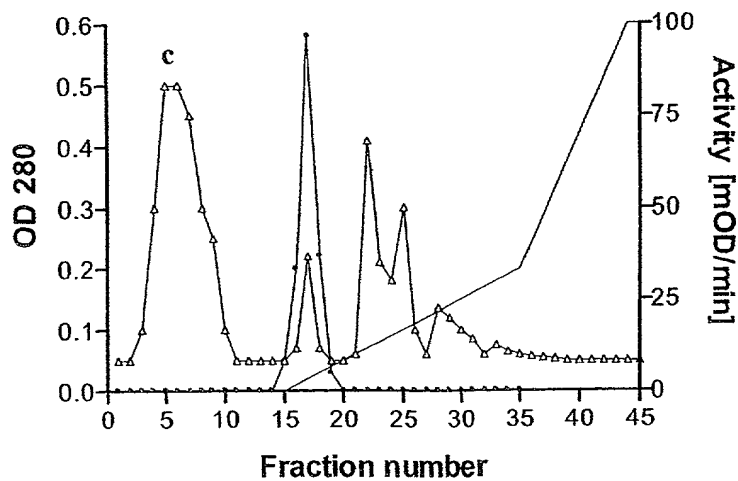
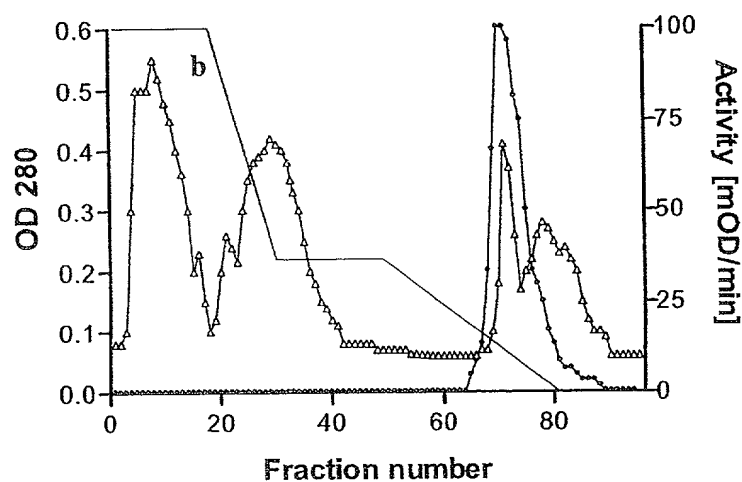
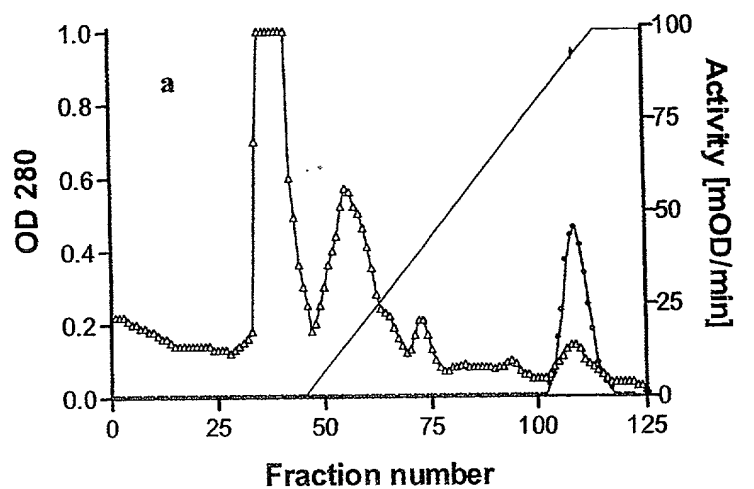


Fig. 2

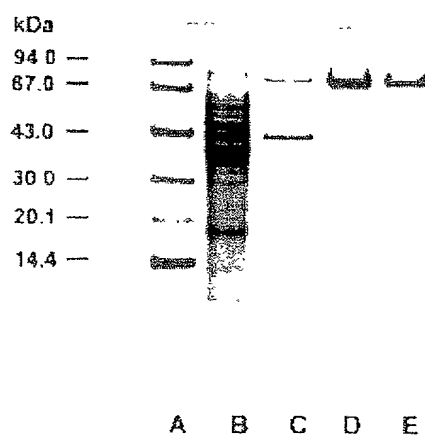
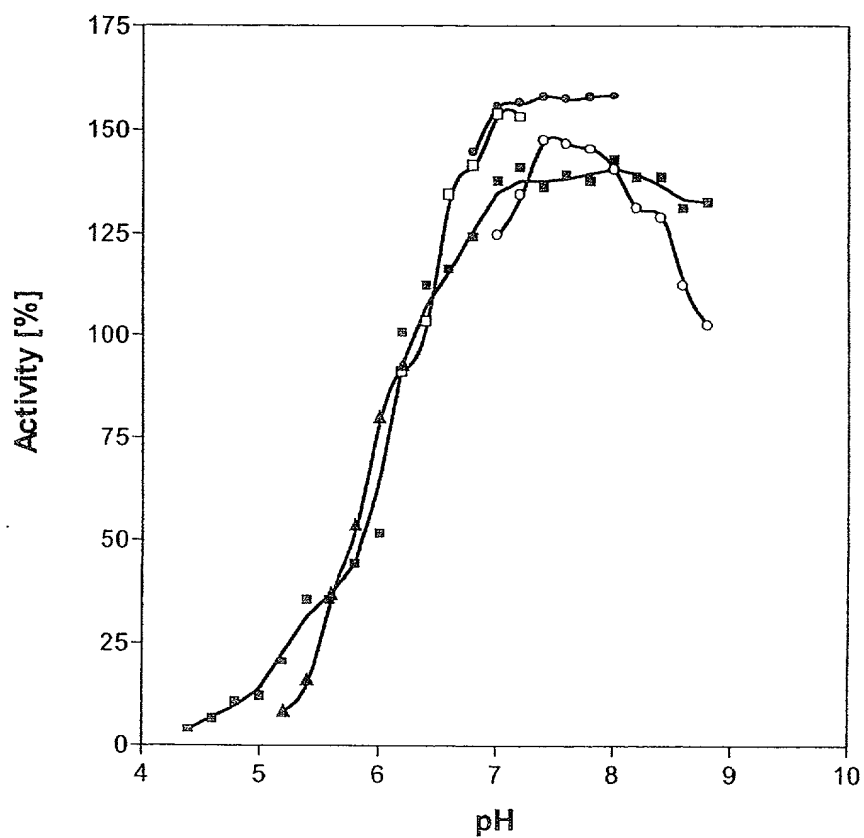


Fig. 3



SRD No. 1  
SRD No. 2

atgcaaatgaaattaaaagattctcttcgcgagcagcctgctgttgggtgcttccagggttagccaaagccgacaaagccatgtggctc	90
<u>M Q M K L K S I L L G A A L L G A S G V A K A D K G M W L</u>	30
ctcaacgaactcaatcaggagaatctggatcgatgcgtgagctcggtcttacgctcccggttgatctctacagtttcgacaagccg	180
<u>L N E L N Q E N L D R M R E L G F T L P L D S L Y S F D K P</u>	60
tccattgccaatgccgtgggttatcttcgggtggcggtatgacccggtatcacagtgtccgatcagggcctgatctttaccaaccaccactgc	270
<u>S I A N A V V I F G G G C T G I T V S D Q G L I F T N H H C</u>	90
ggatacgggtgctatccagagccaaagcaggtgggtacgactatctgcgcgatgggttctgttctcgacagatgggtgaggagcttccg	360
<u>G Y G A I Q S Q S T V D H D Y L R D G F V S R T M G E E L P</u>	120
attccgggtcttttcggtgaagtatctgcgaagatcggtgaaggttaacggacaggtagaaggacagctcaagggtatcactgacgagatg	450
<u>I P G L S V K Y L R K I V K V T D K V E G Q L K G I T D E M</u>	150
gagcgtctgcgcaagctcaggaggtatgccagaactggccaaaaaagaaaatgcagacgagaaccaactctgcatcgtagagcctttc	540
<u>E R L R K A Q E V C Q E L A K K E N A D E N Q L C I V E P F</u>	180
tattccaacaacgaatacttctctatcgctctacgatgtattcaaggacgttcgtatgggtatttgcctctccagctctgtaggttaagttc	630
<u>Y S N N E Y F L I V Y D V F K D V R M V F A P P S S V G K F</u>	210
ggagggcgtacggacaactggatgtggccgctcacacggcgacttcagcgtattccgctgtatgccgggtgccgacaacccggccggcc	720
<u>G G D T D N W M W P R H T G D F S V F R V Y A G A D N R P A</u>	240
gaatacagcaaggacaataaacctataagcccggttacttcgctgcgtatccatgcaaggctacaaggctgacgactatgccatgacc	810
<u>E Y S K D N K P Y K P V Y F A A V S M Q G Y K A D D Y A M T</u>	270
atcggtttcccggtcagtagcgtacgtacctcacttcttgggtgtggaagatcgtagcgaacgagaacaactctcgtagcgaagtt	900
<u>I G F P G S T D R Y L T S W G V E D R I E N E N N P R I E V</u>	300
cgcggtatcaagcaaggcatctggaaggaagccatgagcgcagatcaggctaccggtatcaaatatgccagcaagtagctcagagtgtc	990
<u>R G I K Q G I W K E A M S A D Q A T R I K Y A S K Y A Q S A</u>	330
aactattggaagaattcgatcggtatgaaccgcggtctcgtcgtcttgcagtgataggctcgtaagcgtgccgaggaagagcattcgca	1080
<u>N Y W K N S I G M N R G L A R L D V I G R K R A E E R A F A</u>	360
gactggatccgtaagaacggcaagagtgctgtctatggcgatgtattgtcttctcgaaaaggcctataaggaaggagccaagggccaac	1170
<u>D W I R K N G K S A V Y G D V L S S L E K A Y K E G A K A N</u>	390
cgtagatgacttatttgagcgagacgtcttcgggtggtaccgaggtgggttcggtttgcacagtttgccaacgcattggctacaaatcct	1260
<u>R E M T Y L S E T L F G G T E V V R F A Q F A N A L A T N P</u>	420
gatgctcatgccgtatcctcaaatcgcttgacgacaagtacaagactacctccctcgtctcgaccgtaagggtgctgcccgccatgctc	1350
<u>D A H A G I L K S L D D R Y K D Y L P S L D R K V L P A M L</u>	450
gatattgtacgcggcgatccctgcgacaagctcccgatatttcaagaatgtaatcgacaagaattcaaaaggcgacacgaagaag	1440
<u>D I V R R R I P A D K L P D I F K N V I D K K F K G D T K K</u>	480
tatgcagacttcgtattcgacaagagtggttccctatagcgacaagttccatgccatgctcaagtccttggaaggaaggtttgcc	1530
<u>Y A D F V F D K S V V P Y S D K F H A M L K S M D K E K F A</u>	510
aaggctatcgagaagatccggcagtagagctttccaagagcgtaatagctgctgctgcgctattcaggccgatgcgatggccaatgcc	1620
<u>K A I E K D P A V E L S K S V I A A A R A I Q A D A M A N A</u>	540
tatgccattgagaaggcgcaagcgtcttttcttgcgggtttgcgtgagatgtacccggagcgtgctctgcgagcgatgccaaacttcacc	1710
<u>Y A I E K G K R L F F A G L R E M Y P G R A L P S D A N F T</u>	570
atgcgtatgagctacggctccatcaagggtatgaaccgcaggaaggtgctggtacaactatcatacgacaggcaaggcggtattggag	1800
<u>M R M S Y G S I K G Y E P Q D G A W Y N Y H T T G K G V L E</u>	600
aagcaggatccatgaagagcgatgagtttgcgtacaggagaatatacctcgacctcttcgcacacaaaactatggctcgctatgccgagaac	1890
<u>K Q D P K S D E F A V Q E N I L D L F R T K N Y G R Y A E N</u>	630
ggtagctccatctcgtttctatcgacaacacacatcacggcggttaactccggtagcccggtattcgataagaacggcggtctgctc	1980
<u>G Q L H I A F L S N N D I T G G N S G S P V F D K N G R L I</u>	660
gggtcttgcgttcgatggcaactgggaagctatgagtggtgacatcgagttcgaaaccgatctgcagcgacacacacagcgtggacatccgc	2070
<u>G L A F D G N W E A M S G D I E F E P D L Q R T I S V D I R</u>	690
tacgttctcttcgatgattgacaaatggggcagtgccccgctctcatccaagagctgaagttgatctaa	2139
<u>Y V L F M I D K W G Q C P R L I Q E L K L I *</u>	713

TEBOTT "SEESEBOTT"

Fig. 5

SEQ ID NO: 3 DPP-7	644	TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFFDLQRTISVDIRYVLFM	695
		TGGNSGSPVF++ +IG+ + G +G +	+I + F
SEQ ID NO: 4 V-8	704	TGGNSGSPVFNEKNEVIGIHWGVPNEFNAGVFINENVRNFKQNTIEDIHFA	863

Fig. 6

SEQ ID NO: 5 S1 1 MASQALGFLHONGINTMKKWL SVAVAAAFASHADECMWPHOLP-AMADVLAAGLEHDAKS SKLTFEPMN--AVVSL  
 SEQ ID NO: 6 S2 1 -----MRJIAVAALVLTCCGATADEGQWQYQMP-SHADKLSAHCIDIPAKIADLTSYPMN--AVVGL  
 SEQ ID NO: 7 X 1 -----MRFNLSISVLATLITVDSTHAGECMWVPOOLP-EHAGPLKQAGLO-SPEOISNLIGDEMVG--AVVSL  
 SEQ ID NO: 8 P1 1 -----MQMKLSIHLGAALHLGASGVAKADKGMWFLNELNQENLDRMRELCFTPLPSYFDPKPSHANAVVHFG  
 SEQ ID NO: 9 P2 1 -----MKRILHLPLFAVILCLCQIAHADEGMWLMXOOLG-RKYAQMKEREGKKKEYDYFNPNGTSTKDAVVIFD

78 GGCTASFVSPKGLVWNNHHCAYGSIQVNSTPEKNLLODGFIAKTFADLEPAAPGSRVYNTEDYNTVIERVKA CIENKKG-  
 62 CYCTASVSPQGLVWNNHHCAYKAIQYNKKEHNYLEOCFATSDXEPKPSAGNEPRLVITEAVTDSVTXKDL SQDP--  
 66 CUNCTASLVSPGGLVITNNHHCAYGAIQNLSTPKKNLKEGENALTOADEVSAAGNARIVVEICITDVTQAOKAALAAAGND  
 71 GGCTGITVSDQGLIFTNNHHCYGAIQOSQSTVDHDLRDCGVSRIMC-BELPIPCLSVKYPRKHVKVITPKVECOFKCITD-  
 67 GGCTGEVVSDDRGLVLTNNHHCYGDYMIQAHSTLEHNYLENGEFWAMREA-DELENKDISVVEIDKLEEDVTYVKKDKAIKDP

157 -----REFYQGVENQEKALVAECEDQGYRCQVYSHFGGLEVHLKOLETRDVLVYNPACSVGKXGGVDNNMWPRHT  
 140 -----LKRYEEIENHSHKALIKSCAADNRYRCVNRSHNGLEFVMIKQIMEDVRLVYADPE SVGCGGIDNNYEPHRS  
 146 -----PFKRTTALETFSKOEHAKEEEOGYRCQVYSHFGGLEFVMIKQIMEDVRLVYADPE SVGCGGIDNNYEPHRS  
 149 -----EMERLRKAQEVCOELAKKENADENQOLIVEPEYSNNEVHLVYDVEKDVRYMVAPEPSSVGKFGCDTNNMWPRHT  
 146 NSMDYLSPKYLQKLADKKAGKNSAKNPGLSVEIKAHYGGNVLNFTKKTYTDVRLVYADPEPSSVGKFGCDTNNMWPRHT

231 GDYSFYRAYVSKNGKPAEFSDANNPYEPKPSFLKVSAGVSECDGVNVAGYPCFTNNRYFTATEVQNEFEWAYE EGKMER  
 214 GDFAFILRAYVGDKGPAEFSEDNIPYTPKSLKKNADGVKAGCGVEVAGYPCFTNNRYNLTSFKFASDMLYFTQAKRYOI  
 221 GDFSFRAYVGDKGPAEFSEKNIPYTPKSLKKNADGVKAGCGVEVAGYPCFTNNRYNLTSFKFASDMLYFTQAKRYOI  
 224 GDFSFRAYVGDKGPAEFSEKNIPYTPKSLKKNADGVKAGCGVEVAGYPCFTNNRYNLTSFKFASDMLYFTQAKRYOI  
 226 GDFSFRAYVGDKGPAEFSEKNIPYTPKSLKKNADGVKAGCGVEVAGYPCFTNNRYNLTSFKFASDMLYFTQAKRYOI

311 FIEHIIKATAPEGSDERIKVESQIAGLANVAKNFTSMIEFYGKSTMLADEKALEAKTAETWIAKDS--REAKYKTLAET  
 294 QIDTIEAMGQKQADATIAIKYAGNMASMANMKKLNGLIAGKATDLYGKQORENDFHAWTKNPN-----LNQNLISEL  
 301 LIATIEAASKQNPDIQKYASTIAGNNTSKNFTCQDGHRRINAKCOKOSEETATIAWTKOOCI--RGHEALAAHQTIL  
 304 KQIWEKAMSADQATRIKIVASKYAQSANYWKNSTIGNRLGLADYVIGKRAEERAFADWIRKNGKSAV---YGDVLSLE  
 306 RQGVYIREMLADPOIKIMYSAKYAASONAYKRALCANWALITRGTRONKQAMQDRWANGAKQCTP-----RYEEAVHE

388 DALIAKSKAQHQRDMITSYISSTVMPPTANNLYRLAHEKQLEDMQREPEQDQDNTTRFKASVERIDRRYAAASVDKAVLFD  
 368 EVLLAEQOLOTNTNYFTNAQSSITLTANNLYRLAHEKQLEDMQREPEQDQDNTTRFKASVERIDRRYAAASVDKAVLFD  
 378 VDLTEQYKANQDRDEVTGQNGSGVIGVAVNLYRLAIEETKSDAQREACVQERDLEPTIEGNLKQERRYLPEMDRQYQY  
 381 KAYKEGAKANREMTYLSSETLFGGFEVVRFAAFANALATNPDAHAGILKSLDDKYDYLPSLDKAVLPAMDIVRRTPAD  
 380 IDATVAKRADLRRLMIIIEGIIIRGEIEFARSPIPTEDETKALQNDASRKEAIDKIRTRYSKFANKOYSAEVDKKYAVA

468 MKRYAALPEAQRIEPAQDKAFCIDNKVNEAKLAKTIDKMYAKTEICGNKQVRIAMWKSVDDEKASKDPEIQEAVAMMDTN  
 448 DEN--AYLSQPNRVAALNNMNLNDKN--VSLAAKIDGLYSILITLTDQAQRIAMWEADAKALETSSDPEIIRLAVALYDIN

X 458 WITEYNKIPVKORVAAJIDVWIGDGIPAT-----L-KRLGDTKISSSEERLKMENADRAARESSQDPAIRMAVAIMPAL  
P1 461 KLPDILFNVIDKKFKGDTKKYADFVFD--KS-----VVPYSDFHAKSMKKEKFAKAEKDPANVLSKSVIAAA  
P2 460 MITEYLKEIPYENPLHLRLMKORFAG----DVQAYVDDIFARSVFGSQAQDFAFAVPSVEKLAEDENAVLEASSVEDEY  
  
S1 548 MSEEKKEKELDCEILMKVRPOYMDAIIAANLEQCKPVYADANSSLRVTVCHVKGYSPKDCGFVAVPFTTRLEGIVOKDTG--ID  
S2 524 AOEKAEKILACKLSTARPAHMAAVIDYKANNWPVYPDANGTLRLISYGVVDGYQSRDANKOPFTTRLDGVAKHTG--VE  
X 530 EETERONKIRTCEILKARPITYLOALADYNKSHGKFVYPDANSSLRITTECHVKGYSPKDCGFVAVPFTTRLDGVAKHTG--VE  
P1 530 RAIQADAMANAYAIKCKRLFEAGLREMP--GRALPSDANFTMRMSYCSIKGYEPQDCAWNYHTTTC'GVLEKQDPKSD  
P2 536 RKLYNELRPYDDPILRAQORTYIAGLLEMDG--DQDQEPDANTLRETTYQVKGYSPRDNVAYGHQTTILDGVNKEEDPDNW  
  
S1 627 PEDAPKQOLEHIKQKQYGDYXMKSHDS-----VPVNFLSHTDTTCGNSGSPTENGRAEIVGCLF  
S2 603 PYNAPKLLDAISVQREGDHLVKSUYQDPRGWICRLFSCLDKPEEFNSVPVNFLLSSVDITTCGNSGSPVENGKGLVGLNF  
X 609 PEDSPKSLNAIKAKSYANLADQRIGT-----VPVNFLLSDITTCGNSGSPVLDAGCKLVGLAF  
P1 608 EFVQENLIDLFRTKNYGRVAENGOLH-----IAF--LSNNDITTCGNSGSPVEDKNGELIIGLAF  
P2 614 EFVVDPKIKAVYERKDEGRVADRSRMP-----VAFCAHTTTCGNSGSPVNNANGELIIGLAF  
  
S1 686 DGVYESHICGMAEDNEINRSIHVDTRYMLVMKMYEDHADNLLAEVEIVN-  
S2 683 DSTYEALTKQWFFNPITITRAVHVDIRYLLWMDEVDHADNLIKEDDFVRN  
X 668 DGNWESVSSNNWEDPVMTRTIANDSRVYQWIMTEVAPAPHLIKENIFYR-  
P1 665 DGNWEAMSGDIEFEEDLQRTISVDIRYVLFEMDKW-----  
P2 672 DRNWEVGGDIQYLAZYORSIIVDIRYVILVIDKVGCCQRIIDENNIVP--